

```

1 gcgtctccac cctcagcgg gcggcggtga gtgcgccagg ccagcgccgg cgtgggaccg
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121 gagtttagtg acccttccaa AATGGCTGCT ATTAAGGAAG AGAGAGAGGT GGAAGATTAC
181 AAGAGAAAAA GGAAGACGAT CAGCACAGGC CATGAGCCTA AGGAGCCAGA GCAGTTGAGA
241 AAGCTGTTCA TTGGAGGTCT GAGCTTCGAG ACGACGGATG ATAGCTTGAG AGAGCACTTT
301 GAAAAATGGG GCACACTCAC GGAAGTGTGT GTGATGAGAG ACCCACAAAC AAAACGTTCC
361 AGAGGCTTGG GCTTTGTTAC TTACTCTTGC GTGGAAGAGG TGGATGCGGC CATGAGCGCT
421 CGACCCACATA AGGTGGATGG ACGTGTGGTT GAACCAAGA GAGCAGTTTC AAGGGAGGAT
481 TCTGTAAAGC CTGGGGCGCA TCTCACAGTA AAAAAATAT TTGTTGGTGG CATTAAAGAA
541 GATACAGAAG AATATAATTT AAGGGGTGAC TTGAAACAT ATGGCAAGAT CGAAACGATA
601 GAAATCATGG AAGACAGACA AAGTGGAAAG AAAAGAGGCT TCGCTTTTGT AACTTTTGT
661 GATCAGGATA CAGTTGATAA AATTGTTGTT CAGAAATACC ATACTATAAA TGGTCATAAC
721 TGCGAAGATA AAAAAGCACT CTCAAACAA GAGATGCAGA CTGCCAGCTC TCAGAGAGGT
781 CGTGGGGGTG GTTCAGGCAA CTTCATGGCT CGTGGAAAT TTGAGGTGG TGGAGGAAC
841 TTGGCCGAG GAGGAAACTT TGGTGAAGA GGAGGCTATG GGGGTGGTGG TGGCGTGGT
901 GGGAGCAGAG GAAGCTTTGG GGGTGGTGT GATACAAAC GATTGTTGA TGGTGGCAAC
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1021 TATGGAACC CAGGTGGTGG ATATGAGGT GGAGGAGGAG GATATGGTGG CTACATGAA
1081 GGAGGCAATT TTGGAGGTGG TAATTATGGA GGCAGTGGAA ACTACAATGA CTTTGGTAAC
1141 TACAGTGGAC AGCAGCAGTC CAATTACGGT CCCATGAAAG GTGGTGGCAG TTTTGGTGGT
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1261 GGTGGTAGAA GATTCTaaaa atgctaccag aaaaagggtc acagtcttta gcaggagaga
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1501 gctatttggt aatgcaatgt agtgcgttta gatgtacatc ctgaggtcct tatctgttgt
1561 agctttgtct tcttttttct tttttatttt cccattacat caggtatatt gccctgtaaa
1621 ttgtgttagt ggtaccagga ataaacaaat taaggaattt ttggcttttc aaaaaaaaaa
1681 aaaaaaaaaa

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Fig. 1a

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CHKA1 - MAAIKEEREVEDYKRRKKTISTGHEPKEPEQLRKLFIGGLSFETTDLSLR -50
HUMA1 - M-----SKSESPKEPEQLRKLFIGGLSFETTDLSLR -31

CHKA1 - EQFEKWGLTLDVCVVRDPQTKRSRGFGFVITYSCVEEVDAAARSARPHKVDG -100
HUMA1 - SHFEQWGLTLDVCVVRDPNPKRSRGFGFVITYATVEEVDAAARNARPHKVDG -81

CHKA1 - RVVEPKRAVSREDSVKPGAHLTVKKIFVGGIKEDTEEYNLRGYFETYGKI -150
HUMA1 - RVVEPKRAVSREDSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYGKI -131

CHKA1 - ETIEVMDRQSGKKRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEDEKAL -200
HUMA1 - EVIEIMDRGSGKKRGFAFVTFDDHDSVDKIVIQKYHTVGNHNCVVRKAL -181

CHKA1 - SKQEMQTASS-QRGRGGSGNFMGRGNFGGGG-----NFGRGGNFEGG -242
HUMA1 - SKQEMASASSQRGRSGS-----GNFGGGRGGFGGNDNFGRGNFSG -224

CHKA1 - RGGYGGGGGGSGSGSFGGGDGYNGFGDGGNYGGGPGYGSRGYGGGGGP -292
HUMA1 - RGGFSGSGSGGYGGS---GDGYNGFGNDGS----- -252

CHKA1 - GYGNPGGGYGGGGGYGGYNEGNGFGGNYGGSGNYNDFGNYSQQQQSNY -342
HUMA1 - -----NFGGGGSYNDFGNYNQSS-SNF -273

CHKA1 - GPMKGGSGFGRSSGSPYGGG-----YGSFGSGGGYG-GRRF -378
HUMA1 - GPMKGG-NFGGRSSG-PYGGGGQYFAKPRNQGGYGGSSSSSYSGSGRRF -320

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Fig. 1b

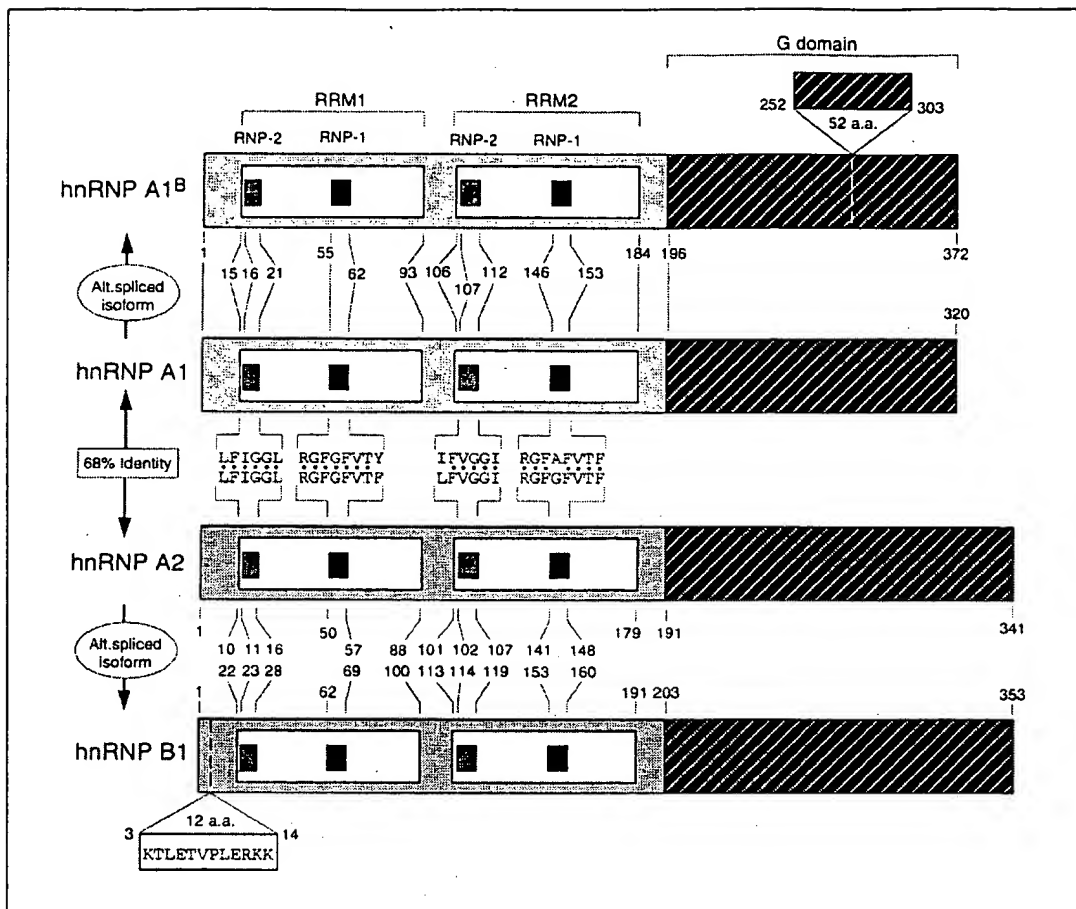


Fig. 2

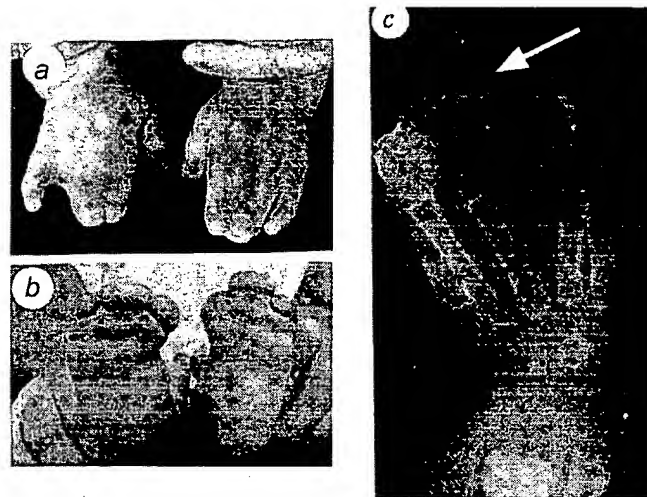


Fig. 3

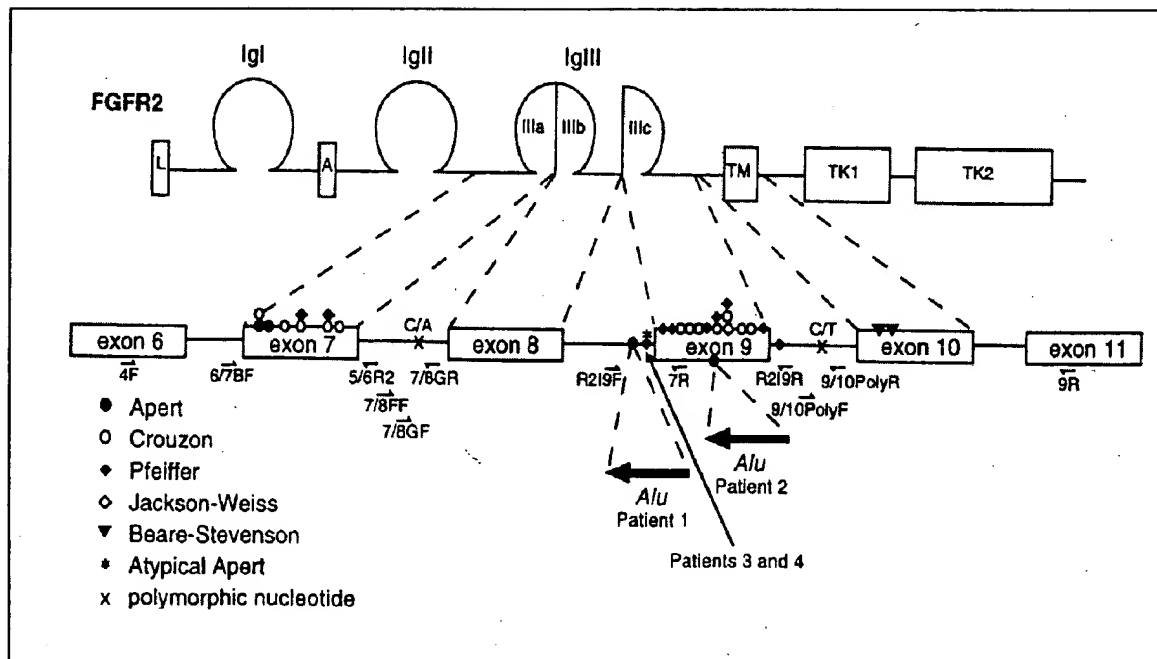
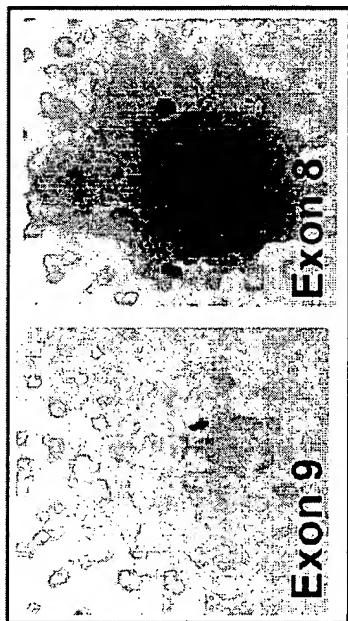
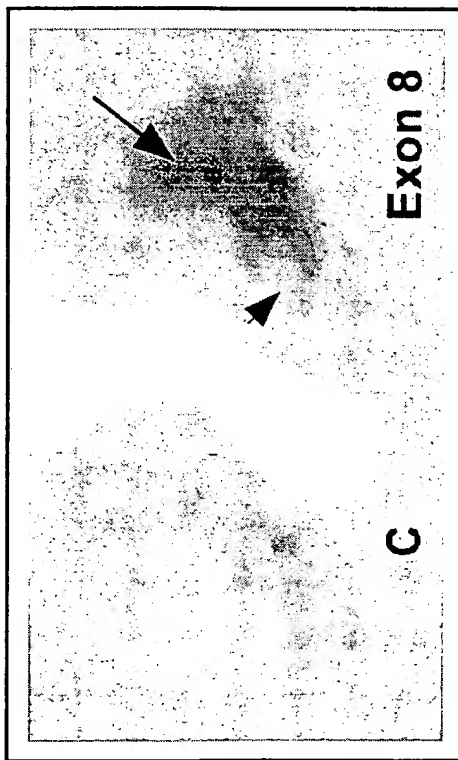


Fig. 4

A.



B.



C.

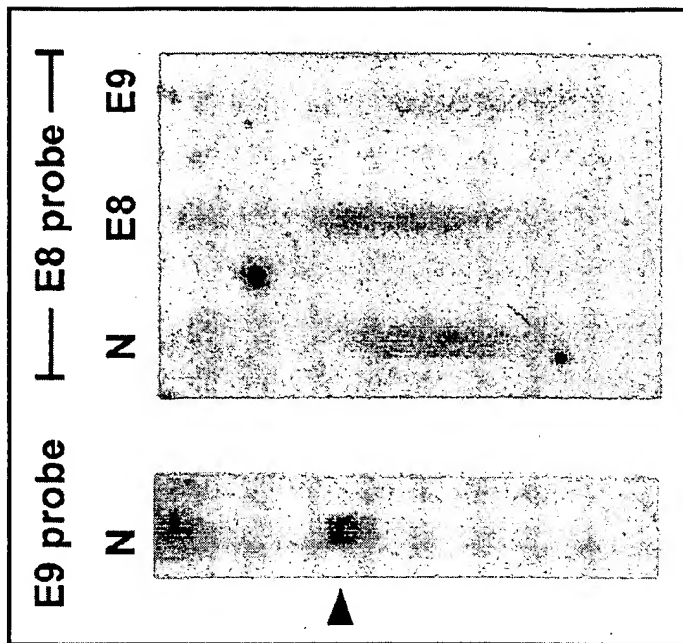


Fig. 5